

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/804,6250590
0607
OIPEDATE: 01/11/2002
TIME: 22:10:28

INPUT SET: S36715.raw

#3

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Wang, Elizabeth A.
Rosen, Vicki A.
Wozney, John M

ENTERED

(ii) TITLE OF INVENTION: Novel BMP Products

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
(B) STREET: 87 CAMBRIDGE PARK DRIVE
(C) CITY: CAMBRIDGE
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/804,625
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/925,779
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: 5160C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-876-1170
(B) TELEFAX: 617-876-5851

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/804,625DATE: 01/11/2002
TIME: 22:10:28

INPUT SET: S36715.raw

47 (2) INFORMATION FOR SEQ ID NO:1:
48
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 592 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: double
53 (D) TOPOLOGY: linear
54
55 (ii) MOLECULE TYPE: DNA (genomic)
56
57 (iii) HYPOTHETICAL: NO
58
59 (iv) ANTI-SENSE: NO
60
61 (vi) ORIGINAL SOURCE:
62 (A) ORGANISM: BOS TAURUS
63
64 (vii) IMMEDIATE SOURCE:
65 (A) LIBRARY: BOVINE GENOMIC IN LAMBDA J1
66 (B) CLONE: LAMBDA BP-21
67
68 (viii) POSITION IN GENOME:
69 (C) UNITS: bp
70
71 (ix) FEATURE:
72 (A) NAME/KEY: CDS
73 (B) LOCATION: 1..390
74
75 (ix) FEATURE:
76 (A) NAME/KEY: mat_peptide
77 (B) LOCATION: 46..387
78
79
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
81
82 GGC CAC GAT GGG AAA GGA CAC CCT CTC CAC AGA AGA GAA AAG CGG CAA 48
83 Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
84 -15 -10 -5 1
85
86 GCA AAA CAC AAA CAG CGG AAA CGC CTC AAG TCC AGC TGT AAG AGA CAC 96
87 Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
88 5 10 15
89
90 CCT TTA TAT GTG GAC TTC AGT GAT GTG GGG TGG AAT GAC TGG ATC GTT 144
91 Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
92 20 25 30
93
94 GCA CCG CCG GGG TAT CAT GCC TTT TAC TGC CAT GGG GAG TGC CCT TTT 192
95 Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
96 35 40 45
97
98 CCC CTG GCC GAT CAC CTT AAC TCC ACG AAT CAT GCC ATT GTC CAA ACT 240
99 Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

DATE: 01/11/2002
TIME: 22:10:28

INPUT SET: S36715.raw

```

100      50              55              60              65
101
102 CTG GTC AAC TCA GTT AAC TCT AAG ATT CCC AAG GCA TGC TGT GTC CCA      288
103 Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
104              70              75              80
105
106 ACA GAG CTC AGC GCC ATC TCC ATG CTG TAC CTT GAT GAG AAT GAG AAG      336
107 Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
108              85              90              95
109
110 GTG GTA TTA AAG AAC TAT CAG GAC ATG GTT GTC GAG GGT TGT GGG TGT      384
111 Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
112              100              105              110
113
114 CGT TAGCACAGCA AAATAAAATA TAAATATATA TATATATATA TTAGAAAAAC      437
115 Arg
116      115
117
118 AGCAAAAAAA TCAAGTTGAC ACTTTAATAT TTCCCAATGA AGACTTTATT TATGGAATGG      497
119
120 AATGGAGAAA AAGAAAAACA CAGCTATTTT GAAAACTATA TTTATATCTA CCGAAAAGAA      557
121
122 GTTGGGAAAA CAAATATTTT AATCAGAGAA TTATT      592
123
124
125 (2) INFORMATION FOR SEQ ID NO:2:
126
127 (i) SEQUENCE CHARACTERISTICS:
128 (A) LENGTH: 129 amino acids
129 (B) TYPE: amino acid
130 (D) TOPOLOGY: linear
131
132 (ii) MOLECULE TYPE: protein
133
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
135
136 Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
137 -15 -10 -5 1
138
139 Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
140 5 10 15
141
142 Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
143 20 25 30
144
145 Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
146 35 40 45
147
148 Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr
149 50 55 60 65
150
151 Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
152 70 75 80

```

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/804,625DATE: 01/11/2002
TIME: 22:10:29

INPUT SET: S36715.raw

153
154 Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
155 85 90 95
156
157 Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
158 100 105 110
159
160 Arg
161
162
163

(2) INFORMATION FOR SEQ ID NO:3:

164
165
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 1607 base pairs
168 (B) TYPE: nucleic acid
169 (C) STRANDEDNESS: double
170 (D) TOPOLOGY: linear
171
172 (ii) MOLECULE TYPE: cDNA to mRNA
173
174 (iii) HYPOTHETICAL: NO
175
176 (iv) ANTI-SENSE: NO
177
178 (vi) ORIGINAL SOURCE:
179 (A) ORGANISM: Homo Sapiens
180 (G) CELL TYPE: Osteosarcoma Cell Line
181 (H) CELL LINE: U-2OS
182
183 (vii) IMMEDIATE SOURCE:
184 (A) LIBRARY: U2OS cDNA in Lambda GT10
185 (B) CLONE: Lambda U2OS-39
186
187 (viii) POSITION IN GENOME:
188 (C) UNITS: bp
189
190 (ix) FEATURE:
191 (A) NAME/KEY: CDS
192 (B) LOCATION: 356..1546
193
194 (ix) FEATURE:
195 (A) NAME/KEY: mat_peptide
196 (B) LOCATION: 1202..1543
197
198 (ix) FEATURE:
199 (A) NAME/KEY: mRNA
200 (B) LOCATION: 14..1607
201
202 (ix) FEATURE:
203 (A) NAME/KEY: sig_peptide
204 (B) LOCATION: 356..424
205

RAW SEQUENCE LISTING PATENT APPLICATION US/09/804,625

DATE: 01/11/2002
TIME: 22:10:29

INPUT SET: S36715.raw

```

206
207      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
208
209      GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT      60
210
211      AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT      120
212
213      CCGAGCCCCA CCGCCCCCTCC ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCACGAC      180
214
215      GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG      240
216
217      GACATTCGGT CCTTGCGCCA GGTCTTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA      300
218
219      ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG      358
220                                     Met
221                                     -282
222
223      GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC      406
224      Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
225      -280                               -275                               -270
226
227      CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC      454
228      Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
229      -265                               -260                               -255                               -250
230
231      GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC      502
232      Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
233      -245                               -240                               -235
234
235      CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG      550
236      Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
237      -230                               -225                               -220
238
239      AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC      598
240      Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
241      -215                               -210                               -205
242
243      CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC      646
244      Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His
245      -200                               -195                               -190
246
247      CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC      694
248      Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His
249      -185                               -180                               -175                               -170
250
251      CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC      742
252      His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr
253      -165                               -160                               -155
254
255      CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC      790
256      Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile
257      -150                               -145                               -140
258

```